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PATENT APPLICATION

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UNITED STATES PATENT AND TRADEMARK OFFICE

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Application No.: 10/517,543 Group: 1637

Filed: July 20, 2005 Examiner: Calamita, Heather

Confirmation No.:9995

For: METHODS FOR DISTINGUISHING RICE VARIETIES

CERTIFICATE OF MAILING OR TRANSMISSION	
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<u>November 6, 2007</u>	
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AMENDMENT AND REPLY TO RESTRICTION REQUIREMENT

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Responsive to the Restriction Requirement dated August 6, 2007, the claims of Group I drawn to a method of distinguishing between rice varieties (new Claims 22-39; see “Amendments to the Claims”) are elected for prosecution. Applicants reserve the right to file a continuing application or take such other appropriate action as deemed necessary to protect the non-elected inventions. Applicants do not hereby abandon or waive any rights in the non-elected inventions.

Responsive to the requirement for an election of a single amino acid sequence or a single nucleic acid sequence for searching purposes, Applicants hereby elect SEQ ID NO:1 as the single nucleic acid sequence.

The requirement is being traversed for the reasons set forth in detail below.

The Examiner stated that the sequences recited in the claims (SEQ ID NOs:1-28) “are patentably distinct because they are unrelated sequences,” and that “the sequence searching in multiple expansive databases has put undue burden on the examiner and office resources.” See the paragraph bridging pages 2 and 3 of the Restriction Requirement. The Examiner further stated in the same paragraph:

For an elected Group drawn to amino acid sequences, the Applicants must further elect a single amino acid sequence. For an elected Group drawn to nucleotide sequences, the Applicants are permitted to elect a single nucleic acid sequence (See MPEP 803.04). (Emphasis in original)

We respectfully disagree with the Examiner and submit that these sequences are not “unrelated” sequences. These sequences are regions of the rice genome that each contain a polymorphism identified as useful for distinguishing rice varieties. Because all sequences originate from the rice genome, they are not “unrelated” sequences.

In addition, as shown in Tables 2 to 7 in the Specification, the claimed method needs an appropriate combination of polymorphisms selected from those in the recited sequences in order to distinguish with certainty among a number of rice varieties. The election of only one sequence would make the method meaningless, or even make it impossible to carry out.

Furthermore, it should be noted that elected Group I is not drawn to amino acid sequences or nucleotide sequences, but to a method of distinguishing between rice varieties using SEQ ID NOs:1-28. MPEP 803.04 addresses nucleotide sequence claims, i.e., composition claims, not method claims. Therefore, MPEP 803.04 is not applicable in the instant case.

In conclusion, Applicants respectfully request that all sequences (SEQ ID NOs:1-28) be examined together.

Responsive to the requirement for an election of species for searching purposes, Applicants hereby elect “g. the method variation of claim 10” as the species.

An extension of time to respond to the Restriction Requirement is respectfully requested. A Petition for an Extension of Time and the appropriate fee are being filed concurrently.

Please amend the application as follows: